

## SEQUENCE LISTING

<110> TOYO BOSEKI KABUSHIKI KAISHA

<120> MODIFIED THERMOSTABLE DNA POLYMERASE

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<150> 2000-138796

<151> 2000-05-11

<160> 28

<170> PatentIn Ver. 2.1

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<212> DNA

<213> Pyrococcus kodakaraensis

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<221> CDS

<222> (156)..(5165)

<223> 1374-2453 intron, 2709-4316 intron

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cctggattgt tctacaagat tatggggat gaaag atg atc ctc gac act gac 173

Met Ile Leu Asp Thr Asp

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tac ata acc gag gat gga aag cct gtc ata aga att ttc aag aag gaa 221

Tyr Ile Thr Glu Asp Gly Lys Pro Val Ile Arg Ile Phe Lys Lys Glu

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aac ggc gag ttt aag att gag tac gac cgg act ttt gaa ccc tac ttc 269

Asn Gly Glu Phe Lys Ile Glu Tyr Asp Arg Thr Phe Glu Pro Tyr Phe

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tac gcc ctc ctg aag gac gat tct gcc att gag gaa gtc aag aag ata 317

Tyr Ala Leu Leu Lys Asp Asp Ser Ala Ile Glu Glu Val Lys Lys Ile

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acc gcc gag agg cac ggg acg gtt gta acg gtt aag cggtt gaa aag 365

Thr Ala Glu Arg His Gly Thr Val Val Thr Val Lys Arg Val Glu Lys

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gtt cag aag aag ttc ctc ggg aga cca gtt gag gtc tgg aaa ctc tac 413

Val Gln Lys Lys Phe Leu Gly Arg Pro Val Glu Val Trp Lys Leu Tyr

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ttt act cat ccg cag gac gtc cca gcg ata agg gac aag ata cga gag 461

Phe Thr His Pro Gln Asp Val Pro Ala Ile Arg Asp Lys Ile Arg Glu

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cat ggg gca gtt att gac atc tac gag tac gac ata ccc ttc gcc aag 509  
 His Gly Ala Val Ile Asp Ile Tyr Glu Tyr Asp Ile Pro Phe Ala Lys

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cgc tac ctc ata gac aag gga tta gtg cca atg gaa ggc gac gag gag 557  
 Arg Tyr Leu Ile Asp Lys Gly Leu Val Pro Met Glu Gly Asp Glu Glu

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ctg aaa atg ctc gcc ttc gac att gaa act ctc tac cat gag ggc gag 605  
 Leu Lys Met Leu Ala Phe Asp Ile Glu Thr Leu Tyr His Glu Gly Glu  
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 Glu Phe Ala Glu Gly Pro Ile Leu Met Ile Ser Tyr Ala Asp Glu Glu

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 Gly Ala Arg Val Ile Thr Trp Lys Asn Val Asp Leu Pro Tyr Val Asp  
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 Val Val Ser Thr Glu Arg Glu Met Ile Lys Arg Phe Leu Arg Val Val  
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aag gag aaa gac ccg gac gtt ctc ata acc tac aac ggc gac aac ttc 797  
 Lys Glu Lys Asp Pro Asp Val Leu Ile Thr Tyr Asn Gly Asp Asn Phe  
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gac ttc gcc tat ctg aaa aag cgc tgt gaa aag ctc gga ata aac ttc 845  
 Asp Phe Ala Tyr Leu Lys Lys Arg Cys Glu Lys Leu Gly Ile Asn Phe  
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gcc ctc gga agg gat gga agc gag ccg aag att cag agg atg ggc gac 893  
 Ala Leu Gly Arg Asp Gly Ser Glu Pro Lys Ile Gln Arg Met Gly Asp  
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agg ttt gcc gtc gaa gtg aag gga cgg ata cac ttc gat ctc tat cct 941  
 Arg Phe Ala Val Glu Val Lys Gly Arg Ile His Phe Asp Leu Tyr Pro  
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gtg ata aga cgg acg ata aac ctg ccc aca tac acg ctt gag gcc gtt 989  
 Val Ile Arg Arg Thr Ile Asn Leu Pro Thr Tyr Thr Leu Glu Ala Val  
 265 270 275

tat gaa gcc gtc ttc ggt cag ccg aag gag aag gtt tac gct gag gaa 1037  
 Tyr Glu Ala Val Phe Gly Gln Pro Lys Glu Lys Val Tyr Ala Glu Glu  
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ata acc aca gcc tgg gaa acc ggc gag aac ctt gag aga gtc gcc cgc			1085
Ile Thr Thr Ala Trp Glu Thr Gly Glu Asn Leu Glu Arg Val Ala Arg			
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tac tcg atg gaa gat gcg aag gtc aca tac gag ctt ggg aag gag ttc			1133
Tyr Ser Met Glu Asp Ala Lys Val Thr Tyr Glu Leu Gly Lys Glu Phe			
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ctt ccg atg gag gcc cag ctt tct cgc tta atc ggc cag tcc ctc tgg			1181
Leu Pro Met Glu Ala Gln Leu Ser Arg Leu Ile Gly Gln Ser Leu Trp			
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gac gtc tcc cgc tcc agc act ggc aac ctc gtt gag tgg ttc ctc ctc			1229
Asp Val Ser Arg Ser Ser Thr Gly Asn Leu Val Glu Trp Phe Leu Leu			
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agg aag gcc tat gag agg aat gag ctg gcc ccg aac aag ccc gat gaa			1277
Arg Lys Ala Tyr Glu Arg Asn Glu Leu Ala Pro Asn Lys Pro Asp Glu			
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aag gag ctg gcc aga aga cgg cag agc tat gaa gga ggc tat gta aaa			1325
Lys Glu Leu Ala Arg Arg Gln Ser Tyr Glu Gly Gly Tyr Val Lys			
375	380	385	390
gag ccc gag aga ggg ttg tgg gag aac ata gtg tac cta gat ttt aga			1373

Glu Pro Glu Arg Gly Leu Trp Glu Asn Ile Val Tyr Leu Asp Phe Arg

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Cys His Pro Ala Asp Thr Lys Val Val Val Lys Gly Lys Gly Ile Ile

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aac atc agc gag gtt cag gaa ggt gac tat gtc ctt ggg att gac ggc 1469

Asn Ile Ser Glu Val Gln Glu Gly Asp Tyr Val Leu Gly Ile Asp Gly

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tgg cag aga gtt aga aaa gta tgg gaa tac gac tac aaa ggg gag ctt 1517

Trp Gln Arg Val Arg Lys Val Trp Glu Tyr Asp Tyr Lys Gly Glu Leu

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gta aac ata aac ggg tta aag tgt acg ccc aat cat aag ctt ccc gtt 1565

Val Asn Ile Asn Gly Leu Lys Cys Thr Pro Asn His Lys Leu Pro Val

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460

465

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gtt aca aag aac gaa cga caa acg aga ata aga gac agt ctt gct aag 1613

Val Thr Lys Asn Glu Arg Gln Thr Arg Ile Arg Asp Ser Leu Ala Lys

475

480

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Ser Phe Leu Thr Lys Lys Val Lys Gly Lys Ile Ile Thr Thr Pro Leu

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gtt ctc aag gga gag ctc gct ggc ata cta ttg gct gaa gga acg ctc    1757 Val Leu Lys Gly Glu Leu Ala Gly Ile Leu Leu Ala Glu Gly Thr Leu			
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ttg agg aaa gac gtt gaa tac ttt gat tca tcc cgc aaa aaa cgg agg    1805 Leu Arg Lys Asp Val Glu Tyr Phe Asp Ser Ser Arg Lys Lys Arg Arg			
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att tca cac cag tat cgt gtt gag ata acc att ggg aaa gac gag gag    1853 Ile Ser His Gln Tyr Arg Val Glu Ile Thr Ile Gly Lys Asp Glu Glu			
555	560	565	
gag ttt agg gat cgt atc aca tac att ttt gag cgt ttg ttt ggg att    1901 Glu Phe Arg Asp Arg Ile Thr Tyr Ile Phe Glu Arg Leu Phe Gly Ile			
570	575	580	
act cca agc atc tcg gag aag aaa gga act aac gca gta aca ctc aaa    1949 Thr Pro Ser Ile Ser Glu Lys Lys Gly Thr Asn Ala Val Thr Leu Lys			
585	590	595	

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ata	gag	tcc	cta	cat	gcc	ccc	tcg	gtt	ctc	agg	gga	ttc	ttc	gaa	ggc	2045
Ile	Glu	Ser	Leu	His	Ala	Pro	Ser	Val	Leu	Arg	Gly	Phe	Phe	Glu	Gly	
615					620					625				630		
gac	ggt	tca	gta	aac	agg	gtt	agg	agg	agt	att	gtt	gca	acc	cag	ggt	2093
Asp	Gly	Ser	Val	Asn	Arg	Val	Arg	Arg	Ser	Ile	Val	Ala	Thr	Gln	Gly	
635					640					645						
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Thr	Lys	Asn	Glu	Trp	Lys	Ile	Lys	Leu	Val	Ser	Lys	Leu	Leu	Ser	Gln	
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ctt	ggt	atc	cct	cat	caa	acg	tac	acg	tat	cag	tat	cag	gaa	aat	ggg	2189
Leu	Gly	Ile	Pro	His	Gln	Thr	Tyr	Thr	Tyr	Gln	Tyr	Gln	Glu	Asn	Gly	
665					670					675						
aaa	gat	cgg	agc	agg	tat	ata	ctg	gag	ata	act	gga	aag	gac	gga	ttg	2237
Lys	Asp	Arg	Ser	Arg	Tyr	Ile	Leu	Glu	Ile	Thr	Gly	Lys	Asp	Gly	Leu	
680					685					690						

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Ile Leu Phe Gln Thr Leu Ile Gly Phe Ile Ser Glu Arg Lys Asn Ala

695 700 705 710

ctg ctt aat aag gca ata tct cag agg gaa atg aac aac ttg gaa aac 2333

Leu Leu Asn Lys Ala Ile Ser Gln Arg Glu Met Asn Asn Leu Glu Asn

715 720 725

aat gga ttt tac agg ctc agt gaa ttc aat gtc agc acg gaa tac tat 2381

Asn Gly Phe Tyr Arg Leu Ser Glu Phe Asn Val Ser Thr Glu Tyr Tyr

730 735 740

gag ggc aag gtc tat gac tta act ctt gaa gga act ccc tac tac ttt 2429

Glu Gly Lys Val Tyr Asp Leu Thr Leu Glu Gly Thr Pro Tyr Tyr Phe

745 750 755

gcc aat ggc ata ttg acc cat aac tcc ctg tac ccc tca atc atc atc 2477

Ala Asn Gly Ile Leu Thr His Asn Ser Leu Tyr Pro Ser Ile Ile Ile

760 765 770

acc cac aac gtc tcg ccg gat acg ctc aac aga gaa gga tgc aag gaa 2525

Thr His Asn Val Ser Pro Asp Thr Leu Asn Arg Glu Gly Cys Lys Glu

775 780 785 790

tat gac gtt gcc cca cag gtc ggc cac cgc ttc tgc aag gac ttc cca 2573

Tyr Asp Val Ala Pro Gln Val Gly His Arg Phe Cys Lys Asp Phe Pro

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gga ttt atc ccg agc ctg ctt gga gac ctc cta gag gag agg cag aag 2621

Gly Phe Ile Pro Ser Leu Leu Gly Asp Leu Leu Glu Glu Arg Gln Lys

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ata aag aag aag atg aag gcc acg att gac ccg atc gag agg aag ctc 2669

Ile Lys Lys Lys Met Lys Ala Thr Ile Asp Pro Ile Glu Arg Lys Leu

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ctc gat tac agg cag agg gcc atc aag atc ctg gca aac agc atc cta 2717

Leu Asp Tyr Arg Gln Arg Ala Ile Lys Ile Leu Ala Asn Ser Ile Leu

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ccc gag gaa tgg ctt cca gtc ctc gag gaa ggg gag gtt cac ttc gtc 2765

Pro Glu Glu Trp Leu Pro Val Leu Glu Glu Gly Glu Val His Phe Val

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agg att gga gag ctc ata gac cgg atg atg gag gaa aat gct ggg aaa 2813

Arg Ile Gly Glu Leu Ile Asp Arg Met Met Glu Glu Asn Ala Gly Lys

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gta aag aga gag ggc gag acg gaa gtg ctt gag gtc agt ggg ctt gaa 2861

Val Lys Arg Glu Gly Glu Thr Glu Val Leu Glu Val Ser Gly Leu Glu

890	895	900	
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905	910	915	
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920	925	930	
<pre> ctg aag tcg ggg agg aga ata aag ata acc tct ggc cac agc ctc ttc      3005 Leu Lys Ser Gly Arg Arg Ile Lys Ile Thr Ser Gly His Ser Leu Phe </pre>			
935	940	945	950
<pre> tct gtg aga aac ggg gag ctc gtt gaa gtt acg ggc gat gaa cta aag      3053 Ser Val Arg Asn Gly Glu Leu Val Glu Val Thr Gly Asp Glu Leu Lys </pre>			
955	960	965	
<pre> cca ggt gac ctc gtt gca gtc ccg cgg aga ttg gag ctt cct gag aga      3101 Pro Gly Asp Leu Val Ala Val Pro Arg Arg Leu Glu Leu Pro Glu Arg </pre>			
970	975	980	
<pre> aac cac gtg ctg aac ctc gtt gaa ctg ctc ctt gga acg cca gaa gaa      3149 Asn His Val Leu Asn Leu Val Glu Leu Leu Leu Gly Thr Pro Glu Glu </pre>			
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Glu Thr Leu Asp Ile Val Met Thr Ile Pro Val Lys Gly Lys Lys Asn

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1005

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Phe Phe Lys Gly Met Leu Arg Thr Leu Arg Trp Ile Phe Gly Glu Glu

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Lys Arg Pro Arg Thr Ala Arg Arg Tyr Leu Arg His Leu Glu Asp Leu

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Gly Tyr Val Arg Leu Lys Lys Ile Gly Tyr Glu Val Leu Asp Trp Asp

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1055

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Ser Leu Lys Asn Tyr Arg Arg Leu Tyr Glu Ala Leu Val Glu Asn Val

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Arg Tyr Asn Gly Asn Lys Arg Glu Tyr Leu Val Glu Phe Asn Ser Ile

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cg<sub>g</sub> gat gca gtt ggc ata atg ccc cta aaa gag ctg aag gag tgg aag 3485  
 Arg Asp Ala Val Gly Ile Met Pro Leu Lys Glu Leu Lys Glu Trp Lys  
 1095 1100 1105 1110

atc ggc acg ctg aac ggc ttc aga atg aga aag ctc att gaa gtg gac 3533  
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gag tcg tta gca aag ctc ctc ggc tac tac gtg agc gag ggc tat gca 3581  
 Glu Ser Leu Ala Lys Leu Leu Gly Tyr Tyr Val Ser Glu Gly Tyr Ala  
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aga aag cag agg aat ccc aaa aac ggc tgg agc tac agc gtg aag ctc 3629  
 Arg Lys Gln Arg Asn Pro Lys Asn Gly Trp Ser Tyr Ser Val Lys Leu  
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tac aac gaa gac cct gaa gtg ctg gac gat atg gag aga ctc gcc agc 3677  
 Tyr Asn Glu Asp Pro Glu Val Leu Asp Asp Met Glu Arg Leu Ala Ser  
 1160 1165 1170

agg ttt ttc ggg aag gtg agg cgg ggc agg aac tac gtt gag ata ccg 3725  
 Arg Phe Phe Gly Lys Val Arg Arg Gly Arg Asn Tyr Val Glu Ile Pro  
 1175 1180 1185 1190

aag aag atc ggc tac ctg ctc ttt gag aac atg tgc ggt gtc cta gcg 3773

Lys Lys Ile Gly Tyr Leu Leu Phe Glu Asn Met Cys Gly Val Leu Ala

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Glu Asn Lys Arg Ile Pro Glu Phe Val Phe Thr Ser Pro Lys Gly Val

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Glu Gln Glu Thr Gln Ala Leu Asn Glu Lys Arg Ala Leu Ala Asn Gln

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cic gtc ctc ctc ttg aac tcg gtg ggg gtc tct gct gta aaa ctt ggg 3965

Leu Val Leu Leu Asn Ser Val Gly Val Ser Ala Val Lys Leu Gly

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Val Lys Leu Asp Lys Lys Lys Asn Ala Tyr Tyr Ser His Val Ile Pro

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aag gaa gtc ctg agc gag gtc ttt ggg aag gtt ttc cag aaa aac gtc 4109  
 Lys Glu Val Leu Ser Glu Val Phe Gly Lys Val Phe Gln Lys Asn Val

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 Asp Arg Val Glu Ser Val Asp Val Glu Asp Tyr Asp Gly Tyr Val Tyr

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 Asp Leu Ser Val Glu Asp Asn Glu Asn Phe Leu Val Gly Phe Gly Leu

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gtc tat gct cac aac agc tac tac ggt tac tac ggc tat gca agg gcg 4349  
 Val Tyr Ala His Asn Ser Tyr Tyr Gly Tyr Tyr Gly Tyr Ala Arg Ala

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cgc tgg tac tgc aag gag tgt gca gag agc gta acg gcc tgg gga agg 4397  
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 Glu Tyr Ile Thr Met Thr Ile Lys Glu Ile Glu Glu Lys Tyr Gly Phe  
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aag gta atc tac agc gac acc gac gga ttt ttt gcc aca ata cct gga 4493  
 Lys Val Ile Tyr Ser Asp Thr Asp Gly Phe Phe Ala Thr Ile Pro Gly  
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gcc gat gct gaa acc gtc aaa aag aag gct atg gag ttc ctc aag tat 4541  
 Ala Asp Ala Glu Thr Val Lys Lys Lys Ala Met Glu Phe Leu Lys Tyr  
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atc aac gcc aaa ctt ccg ggc gcg ctt gag ctc gag tac gag ggc ttc 4589  
 Ile Asn Ala Lys Leu Pro Gly Ala Leu Glu Leu Glu Tyr Glu Gly Phe  
 1465 1470 1475

tac aaa cgc ggc ttc ttc gtc acg aag aag aag tat gcg gtg ata gac 4637  
 Tyr Lys Arg Gly Phe Phe Val Thr Lys Lys Tyr Ala Val Ile Asp  
 1480 1485 1490

DRAFT GENOME SEQUENCING PROJECT

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tgg agc gag ata gcg aaa gag acg cag gcg agg gtt ctt gaa gct ttg 4733

Trp Ser Glu Ile Ala Lys Glu Thr Gln Ala Arg Val Leu Glu Ala Leu

1515 1520 1525

cta aag gac ggt gac gtc gag aag gcc gtg agg ata gtc aaa gaa gtt 4781

Leu Lys Asp Gly Asp Val Glu Lys Ala Val Arg Ile Val Lys Glu Val

1530 1535 1540

acc gaa aag ctg agc aag tac gag gtt ccg ccg gag aag ctg gtg atc 4829

Thr Glu Lys Leu Ser Lys Tyr Glu Val Pro Pro Glu Lys Leu Val Ile

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cac gag cag ata acg agg gat tta aag gac tac aag gca acc ggt ccc 4877

His Glu Gln Ile Thr Arg Asp Leu Lys Asp Tyr Lys Ala Thr Gly Pro

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cac gtt gcc gtt gcc aag agg ttg gcc gcg aga gga gtc aaa ata cgc 4925

His Val Ala Val Ala Lys Arg Leu Ala Ala Arg Gly Val Lys Ile Arg

1575 1580 1585 1590

cct gga acg gtg ata agc tac atc gtg ctc aag ggc tct ggg agg ata 4973

Pro Gly Thr Val Ile Ser Tyr Ile Val Leu Lys Gly Ser Gly Arg Ile

1595

1600

1605

ggc gac agg gcg ata ccg ttc gac gag ttc gac ccg acg aag cac aag 5021

Gly Asp Arg Ala Ile Pro Phe Asp Glu Phe Asp Pro Thr Lys His Lys

1610

1615

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tac gac gcc gag tac tac att gag aac cag gtt ctc cca gcc gtt gag 5069

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aga att ctg aga gcc ttc ggt tac cgc aag gaa gac ctg cgc tac cag 5117

Arg Ile Leu Arg Ala Phe Gly Tyr Arg Lys Glu Asp Leu Arg Tyr Gln

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aag acg aga cag gtt ggt ttg agt gct tgg ctg aag ccg aag gga act 5165

Lys Thr Arg Gln Val Gly Leu Ser Ala Trp Leu Lys Pro Lys Gly Thr

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1

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30

Thr Phe Glu Pro Tyr Phe Tyr Ala Leu Leu Lys Asp Asp Ser Ala Ile

35

40

45

Glu Glu Val Lys Lys Ile Thr Ala Glu Arg His Gly Thr Val Val Thr

50

55

60

Val Lys Arg Val Glu Lys Val Gln Lys Lys Phe Leu Gly Arg Pro Val

65

70

75

80

Glu Val Trp Lys Leu Tyr Phe Thr His Pro Gln Asp Val Pro Ala Ile

85

90

95

Arg Asp Lys Ile Arg Glu His Pro Ala Val Ile Asp Ile Tyr Glu Tyr

100

105

110

Asp Ile Pro Phe Ala Lys Arg Tyr Leu Ile Asp Lys Gly Leu Val Pro

115

120

125

Met Glu Gly Asp Glu Glu Leu Lys Met Leu Ala Phe Asp Ile Glu Thr

130

135

140

Leu Tyr His Glu Gly Glu Glu Phe Ala Glu Gly Pro Ile Leu Met Ile

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Ser Tyr Ala Asp Glu Glu Gly Ala Arg Val Ile Thr Trp Lys Asn Val

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175

Asp Leu Pro Tyr Val Asp Val Val Ser Thr Glu Arg Glu Met Ile Lys

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Arg Phe Leu Arg Val Val Lys Glu Lys Asp Pro Asp Val Leu Ile Thr

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Tyr Asn Gly Asp Asn Phe Asp Phe Ala Tyr Leu Lys Lys Arg Cys Glu

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Lys Leu Gly Ile Asn Phe Ala Leu Gly Arg Asp Gly Ser Glu Pro Lys

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His Phe Asp Leu Tyr Pro Val Ile Arg Arg Thr Ile Asn Leu Pro Thr

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Tyr Thr Leu Glu Ala Val Tyr Glu Ala Val Phe Gly Gln Pro Lys Glu

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290

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Leu Glu Arg Val Ala Arg Tyr Ser Met Glu Asp Ala Lys Val Thr Tyr

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Glu Leu Gly Lys Glu Phe Leu Pro Met Glu Ala Gln Leu Ser Arg Leu

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Ile Gly Gln Ser Leu Trp Asp Val Ser Arg Ser Ser Thr Gly Asn Leu

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Val Glu Trp Phe Leu Leu Arg Lys Ala Tyr Glu Arg Asn Glu Leu Ala

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360

365

Pro Asn Lys Pro Asp Glu Lys Glu Leu Ala Arg Arg Arg Gln Ser Tyr

370 375 380

Glu Gly Gly Tyr Val Lys Glu Pro Glu Arg Gly Leu Trp Glu Asn Ile

385 390 395 400

Val Tyr Leu Asp Phe Arg Ser Leu Tyr Pro Ser Ile Ile Ile Thr His

405 410 415

Asn Val Ser Pro Asp Thr Leu Asn Arg Glu Gly Cys Lys Glu Tyr Asp

420 425 430

Val Ala Pro Gln Val Gly His Arg Phe Cys Lys Asp Phe Pro Gly Phe

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Ile Pro Ser Leu Leu Gly Asp Leu Leu Glu Glu Arg Gln Lys Ile Lys

450 455 460

Lys Lys Met Lys Ala Thr Ile Asp Pro Ile Glu Arg Lys Leu Leu Asp

465 470 475 480

Tyr Arg Gln Arg Ala Ile Lys Ile Leu Ala Asn Ser Tyr Tyr Gly Tyr

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Tyr Gly Tyr Ala Arg Ala Arg Trp Tyr Cys Lys Glu Cys Ala Glu Ser

500

505

510

Val Thr Ala Trp Gly Arg Glu Tyr Ile Thr Met Thr Ile Lys Glu Ile

515

520

525

Glu Glu Lys Tyr Gly Phe Lys Val Ile Tyr Ser Asp Thr Asp Gly Phe

530

535

540

Phe Ala Thr Ile Pro Gly Ala Asp Ala Glu Thr Val Lys Lys Lys Ala

545

550

555

560

Met Glu Phe Leu Lys Tyr Ile Asn Ala Lys Leu Pro Gly Ala Leu Glu

565

570

575

Leu Glu Tyr Glu Gly Phe Tyr Lys Arg Gly Phe Phe Val Thr Lys Lys

580

585

590

Lys Tyr Ala Val Ile Asp Glu Glu Gly Lys Ile Thr Thr Arg Gly Leu

595

600

605

Glu Ile Val Arg Arg Asp Trp Ser Glu Ile Ala Lys Glu Thr Gln Ala

610

615

620

Arg Val Leu Glu Ala Leu Leu Lys Asp Gly Asp Val Glu Lys Ala Val

625

630

635

640

Arg Ile Val Lys Glu Val Thr Glu Lys Leu Ser Lys Tyr Glu Val Pro

645

650

655

Pro Glu Lys Leu Val Ile His Glu Gln Ile Thr Arg Asp Leu Lys Asp

660

665

670

Tyr Lys Ala Thr Gly Pro His Val Ala Val Ala Lys Arg Leu Ala Ala

675

680

685

Arg Gly Val Lys Ile Arg Pro Gly Thr Val Ile Ser Tyr Ile Val Leu

690

695

700

Lys Gly Ser Gly Arg Ile Gly Asp Arg Ala Ile Pro Phe Asp Glu Phe

705

710

715

720

Asp Pro Thr Lys His Lys Tyr Asp Ala Glu Tyr Tyr Ile Glu Asn Gln

725

730

735

Val Leu Pro Ala Val Glu Arg Ile Leu Arg Ala Phe Gly Tyr Arg Lys

740

745

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Glu Asp Leu Arg Tyr Gln Lys Thr Arg Gln Val Gly Leu Ser Ala Trp

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Leu Lys Pro Lys Gly Thr

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<210> 18

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